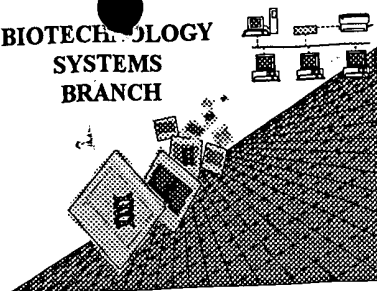


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/852,058
Source: 01PE
Date Processed by STIC: 10/10/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/852,058

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics
_____ Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 _____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 _____ Misaligned Amino
_____ Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 _____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 _____ PatentIn 2.0
_____ "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 _____ Skipped Sequences
_____ (OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 _____ Skipped Sequences
_____ (NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 _____ Use of n's or Xaa's
_____ (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 _____ Invalid <213>
_____ Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 _____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 _____ PatentIn 2.0
_____ "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 _____ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/852,058

DATE: 10/10/2001
 TIME: 17:07:04

Input Set : A:\2404640.diatech.method.ST25.txt
 Output Set: N:\CRF3\10102001\I852058.raw

Does Not Comply
 Corrected Diskette Needed

pg 1-4

etc

3 <110> APPLICANT: Diatech Pty. Ltd.
 5 <120> TITLE OF INVENTION: A method
 7 <130> FILE REFERENCE: 2404640/EJH
 9 <140> CURRENT APPLICATION NUMBER: US/09/852,058
 9 <141> CURRENT FILING DATE: 2001-08-13
 9 <150> PRIOR APPLICATION NUMBER: US 60/202,797
 10 <151> PRIOR FILING DATE: 2000-05-09
 12 <160> NUMBER OF SEQ ID NOS: 26
 14 <170> SOFTWARE: PatentIn version 3.0

16 <210> SEQ ID NO: 1

17 <211> LENGTH: 18

18 <212> TYPE: DNA

19 <213> ORGANISM: primer

21 <400> SEQUENCE: 1

22 cagatccctg gacagcg

25 <210> SEQ ID NO: 2

26 <211> LENGTH: 18

27 <212> TYPE: DNA

28 <213> ORGANISM: primer

30 <400> SEQUENCE: 2

31 cagatccctg gacaggca

34 <210> SEQ ID NO: 3

35 <211> LENGTH: 83

36 <212> TYPE: DNA

37 <213> ORGANISM: primer

39 <400> SEQUENCE: 3

40 aggaatacag gtattttgtc cttgcgcggt gagctatatg gggactatga atttctaata

42 ggactacttc taatctgtaa gag

45 <210> SEQ ID NO: 4

46 <211> LENGTH: 20

47 <212> TYPE: DNA

48 <213> ORGANISM: primer

50 <400> SEQUENCE: 4

51 aatctgtaag agcagatccc

54 <210> SEQ ID NO: 5

55 <211> LENGTH: 29

56 <212> TYPE: DNA

57 <213> ORGANISM: primer

59 <400> SEQUENCE: 5

60 tttttttttt gtcccatat agctcaccg

63 <210> SEQ ID NO: 6

64 <211> LENGTH: 18

65 <212> TYPE: DNA

66 <213> ORGANISM: primer

68 <400> SEQUENCE: 6

69 cagatccctg gacagacg

72 <210> SEQ ID NO: 7

18

18

60

83

20

29

18

see item 10 on Ena Summary Sheet
 (global error)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/852,058

DATE: 10/10/2001

TIME: 17:07:04

Input Set : A:\2404640.diatech.method.ST25.txt

Output Set: N:\CRF3\10102001\I852058.raw

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78 cagatccctg gacagaca 18
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83 <212> TYPE: DNA
84 <213> ORGANISM: primer
86 <400> SEQUENCE: 8
87 gatccctgga cagacg 16
90 <210> SEQ ID NO: 9
91 <211> LENGTH: 16
92 <212> TYPE: DNA
93 <213> ORGANISM: primer
95 <400> SEQUENCE: 9
96 gatccctgga cagaca 16
99 <210> SEQ ID NO: 10
100 <211> LENGTH: 22
101 <212> TYPE: DNA
102 <213> ORGANISM: primer
104 <400> SEQUENCE: 10
105 tgcccagtg c ttaacaagac ca 22
108 <210> SEQ ID NO: 11
109 <211> LENGTH: 20
110 <212> TYPE: DNA
111 <213> ORGANISM: primer
113 <400> SEQUENCE: 11
114 tgttatcaca ctggtgctaa 20
117 <210> SEQ ID NO: 12
118 <211> LENGTH: 67
119 <212> TYPE: DNA
120 <213> ORGANISM: primer
122 <400> SEQUENCE: 12
123 gcaggtaaag aaggcgccgc ggtgagctat atggggacta tgaatttgct ccattaaagc 60
125 aaattgc 67
128 <210> SEQ ID NO: 13
129 <211> LENGTH: 49
130 <212> TYPE: DNA
131 <213> ORGANISM: primer
133 <400> SEQUENCE: 13
134 atagcgccctt ctttacctgc gttacttcga atttgcttta atggagctg 49
137 <210> SEQ ID NO: 14
138 <211> LENGTH: 7
139 <212> TYPE: DNA
140 <213> ORGANISM: primer
142 <400> SEQUENCE: 14
143 aagtaac 7
146 <210> SEQ ID NO: 15

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/852,058

DATE: 10/10/2001

TIME: 17:07:04

Input Set : A:\2404640.diatech.method.ST25.txt

Output Set: N:\CRF3\10102001\I852058.raw

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155 <210> SEQ ID NO: 16
156 <211> LENGTH: 7
157 <212> TYPE: DNA
158 <213> ORGANISM: primer
160 <400> SEQUENCE: 16
161 tgcaaac 7
164 <210> SEQ ID NO: 17
165 <211> LENGTH: 20
166 <212> TYPE: DNA
167 <213> ORGANISM: primer
169 <400> SEQUENCE: 17
170 ccattaaagc aaattgcaag 20
173 <210> SEQ ID NO: 18
174 <211> LENGTH: 21
175 <212> TYPE: DNA
176 <213> ORGANISM: primer
178 <400> SEQUENCE: 18
179 ccattaaagc aaattgctgc a 21
182 <210> SEQ ID NO: 19
183 <211> LENGTH: 18
184 <212> TYPE: DNA
185 <213> ORGANISM: primer
187 <400> SEQUENCE: 19
188 cagatccctg gacaggcg 18
191 <210> SEQ ID NO: 20
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193 <212> TYPE: DNA
194 <213> ORGANISM: primer
196 <400> SEQUENCE: 20
197 cagatccctg gacaggca 18
200 <210> SEQ ID NO: 21
201 <211> LENGTH: 25
202 <212> TYPE: DNA
203 <213> ORGANISM: primer
205 <400> SEQUENCE: 21
206 tgtagagcat tacgctgcga tggat 25
209 <210> SEQ ID NO: 22
210 <211> LENGTH: 20
211 <212> TYPE: DNA
212 <213> ORGANISM: primer
214 <400> SEQUENCE: 22
215 tgatgctcca taacttcctg 20
218 <210> SEQ ID NO: 23
219 <211> LENGTH: 13

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/852,058

DATE: 10/10/2001

TIME: 17:07:04

Input Set : A:\2404640.diatech.method.ST25.txt

Output Set: N:\CRF3\10102001\I852058.raw

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221 <213> ORGANISM: primer
223 <400> SEQUENCE: 23
224 ctgtggaatt gag 13
227 <210> SEQ ID NO: 24
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229 <212> TYPE: DNA
230 <213> ORGANISM: primer
232 <400> SEQUENCE: 24
233 ctgtggaatt gag 13
236 <210> SEQ ID NO: 25
237 <211> LENGTH: 13
238 <212> TYPE: DNA
239 <213> ORGANISM: primer
241 <400> SEQUENCE: 25
242 ctctggaatt gat 13
245 <210> SEQ ID NO: 26
246 <211> LENGTH: 30
247 <212> TYPE: DNA
248 <213> ORGANISM: primer
250 <400> SEQUENCE: 26
251 atcgcgaaaa ctgtggaatt gatcagcggt 30

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/852,058

DATE: 10/10/2001

TIME: 17:07:05

Input Set : A:\2404640.diatech.method.ST25.txt

Output Set: N:\CRF3\10102001\I852058.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date